

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/479,240DATE: 02/01/2000
TIME: 23:28:19

INPUT SET: S34590.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

- 1
2
3 (1) General Information:
4
5 (i) APPLICANT: KLEIN, Michel H
6 DU, Run-Pan
7 EWASYSHYN, Mary E
8
9 (ii) TITLE OF INVENTION: INFECTION DETECTION METHOD USING
10 CHIMERIC PROTEIN
11
12 (iii) NUMBER OF SEQUENCES: 38
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Sim & McBurney
16 (B) STREET: 6th Floor, 330 University Avenue
17 (C) CITY: Toronto
18 (D) STATE: Ontario
19 (E) COUNTRY: Canada
20 (F) ZIP: M5G 1R7
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER:
30 (B) FILING DATE:
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US 08/467,961
35 (B) FILING DATE: 06-JUN-1995
36
37 (vii) PRIOR APPLICATION DATA:
38 (A) APPLICATION NUMBER: US 08/001,554
39 (B) FILING DATE: 06-JAN-1993
40
41 (vii) PRIOR APPLICATION DATA:
42 (A) APPLICATION NUMBER: GB 9200117.1
43 (B) FILING DATE: 06-JAN-1992
44
45 (viii) ATTORNEY/AGENT INFORMATION:
46 (A) NAME: STEWART, Michael I

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47 (B) REGISTRATION NUMBER: 24,973
48 (C) REFERENCE/DOCKET NUMBER: 1038-1000 MIS:jb
49
50 (ix) TELECOMMUNICATION INFORMATION:
51 (A) TELEPHONE: (416) 595-1155
52 (B) TELEFAX: (416) 595-1163
53
54
55 (2) INFORMATION FOR SEQ ID NO:1:
56
57 (i) SEQUENCE CHARACTERISTICS:
58 (A) LENGTH: 1844 base pairs
59 (B) TYPE: nucleic acid
60 (C) STRANDEDNESS: single
61 (D) TOPOLOGY: linear
62
63 (ii) MOLECULE TYPE: DNA (genomic)
64
65
66
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
68
69 AAGTCAATAC CAACAACATAT TAGCAGTCAT ACGTGCAAGA ACAAGAAAGA AGAGATTCAA 60
70
71 AAAGCTAAAT AAGAGAAATC AAAACAAAAG GTATAGAACA CCCGAACAAC AAAATCAAAA 120
72
73 CATCCAATCC ATTTTAAACA AAAATTCCAA AAGAGACCGG CAACACAACA AGCACCAAAC 180
74
75 ACAATGCCAA CTTTAATACT GCTAATTATT ACAACAATGA TTATGGCATC TTCCTGCCAA 240
76
77 ATAGATATCA CAAAACTACA GCATGTAGGT GTATTGGTCA ACAGTCCCAA AGGGATGAAG 300
78
79 ATATCACAAA ACTTCGAAAC AAGATATCTA ATTTTGAGCC TCATACCAA AATAGAAGAC 360
80
81 TCTAACTCTT GTGGTGACCA ACAGATCAAA CAATACAAGA GGTTATTGGA TAGACTGATC 420
82
83 ATCCCTCTAT ATGATGGATT AAGATTACAG AAAGATGTGA TAGTAACCAA TCAAGAATCC 480
84
85 AATGAAAACA CTGATCCCAG AACAAGACGA TCCTTTGGAG GGGTAATTGG AACCATTGCT 540
86
87 CTGGGAGTAG CAACCTCAGC ACAAATTACA GCGGCAGTTG CTCTGGTTGA AGCCAAGCAG 600
88
89 GCAAAATCAG ACATCGAAAA ACTCAAAGAA GCAATCAGGG ACACAAACAA AGCAGTGCAG 660
90
91 TCAGTTCAGA GCTCTATAGG AAATTTAATA GTAGCAATTA AATCAGTCCA AGATTATGTC 720
92
93 AACAACGAAA TGGTGCCATC GATTGCTAGA CTAGGTTGTG AAGCAGCAGG ACTTCAATTA 780
94
95 GGAATTGCAT TAACACAGCA TTAATCAGAA TTAACAAACA TATTTGGTGA TAACATAGGA 840
96
97 TCGTTACAAG AAAAAGGAAT AAAATTACAA GGTATAGCAT CATTATACCG CACAAATATC 900
98
99 ACAGAAATAT TCACAACATC AACAGTTGAT AAATATGATA TCTATGATCT ATTATTTACA 960

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100
101 GAATCAATAA AGGTGAGAGT TATAGATGTT GATTTGAATG ATTACTCAAT CACCCTCCAA 1020
102
103 GTCAGACTCC CTTTATTAAC TAGGCTGCTG AACACTCAGA TCTACAAAGT AGATTCCATA 1080
104
105 TCATATAATA TCCAAAACAG AGAATGGTAT ATCCCTCTTC CCAGCCATAT CATGACGAAA 1140
106
107 GGGGCATTTC TAGGTGGAGC AGATGTCAAG GAATGTATAG AAGCATTTCAG CAGTTATATA 1200
108
109 TGCCCTTCTG ATCCAGGATT TGTACTAAAC CATGAAATGG AGAGCTGCTT ATCAGGAAAC 1260
110
111 ATATCCCAAT GTCCAAGAAC CACGGTCACA TCAGACATTG TTCCAAGATA TGCATTTGTC 1320
112
113 AATGGAGGAG TGGTTGCAAA CTGTATAACA ACCACCTGTA CATGCAACGG AATCGACAAT 1380
114
115 AGAATCAATC AACCACCTGA TCAAGGAGTA AAAATTATAA CACATAAAGA ATGTAATACA 1440
116
117 ATAGGTATCA ACGGAATGCT GTTCAATACA AATAAAGAAG GAACTCTTGC ATTCTACACA 1500
118
119 CCAAATGATA TAACACTAAA TAATTCTGTT GCACTTGATC CAATTGACAT ATCAATCGAG 1560
120
121 CTTAACAAAG CCAAATCAGA TCTAGAAGAA TCAAAAGAAT GGATAAGAAG GTCAAATCAA 1620
122
123 AAAC TAGATT CTATTGGAAA CTGGCATCAA TCTAGCACTA CAATCATAAT TATTTTAATA 1680
124
125 ATGATCATT TAATTGTTTAT AATTAATGTA ACGATAATTA CAATTGCAAT TAAGTATTAC 1740
126
127 AGAATTCAAA AGAGAAATCG AGTGGATCAA AATGACAAGC CATATGTACT AACAAACAAA 1800
128
129 TGACATATCT ATAGATCATT AGATATTAAA ATTATAAAAA ACTT 1844
130
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
141 Met Pro Thr Leu Ile Leu Leu Ile Ile Thr Thr Met Ile Met Ala Ser
142 1 5 10 15
143 Ser Cys Gln Ile Asp Ile Thr Lys Leu Gln His Val Gly Val Leu Val
144 20 25 30
145 Asn Ser Pro Lys Gly Met Lys Ile Ser Gln Asn Phe Glu Thr Arg Tyr
146 35 40 45
147 Leu Ile Leu Ser Leu Ile Pro Lys Ile Glu Asp Ser Asn Ser Cys Gly
148
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153	50	55	60
154			
155	Asp Gln Gln Ile Lys Gln Tyr Lys Arg Leu Leu Asp Arg Leu Ile Ile		
156	65	70	75 80
157			
158	Pro Leu Tyr Asp Gly Leu Arg Leu Gln Lys Asp Val Ile Val Thr Asn		
159		85	90 95
160			
161	Gln Glu Ser Asn Glu Asn Thr Asp Pro Arg Thr Arg Arg Ser Phe Gly		
162		100	105 110
163			
164	Gly Val Ile Gly Thr Ile Ala Leu Gly Val Ala Thr Ser Ala Gln Ile		
165		115	120 125
166			
167	Thr Ala Ala Val Ala Leu Val Glu Ala Lys Gln Ala Lys Ser Asp Ile		
168		130	135 140
169			
170	Glu Lys Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser		
171		145	150 155 160
172			
173	Val Gln Ser Ser Ile Gly Asn Leu Ile Val Ala Ile Lys Ser Val Gln		
174		165	170 175
175			
176	Asp Tyr Val Asn Asn Glu Ile Val Pro Ser Ile Ala Arg Leu Gly Cys		
177		180	185 190
178			
179	Glu Ala Ala Gly Leu Gln Leu Gly Ile Ala Leu Thr Gln His Tyr Ser		
180		195	200 205
181			
182	Glu Leu Thr Asn Ile Phe Gly Asp Asn Ile Gly Ser Leu Gln Glu Lys		
183		210	215 220
184			
185	Gly Ile Lys Leu Gln Gly Ile Ala Ser Leu Tyr Arg Thr Asn Ile Thr		
186		225	230 235 240
187			
188	Glu Ile Phe Thr Thr Ser Thr Val Asp Lys Tyr Asp Ile Tyr Asp Leu		
189		245	250 255
190			
191	Leu Phe Thr Glu Ser Ile Lys Val Arg Val Ile Asp Val Asp Leu Asn		
192		260	265 270
193			
194	Asp Tyr Ser Ile Thr Leu Gln Val Arg Leu Pro Leu Leu Thr Arg Leu		
195		275	280 285
196			
197	Leu Asn Thr Gln Ile Tyr Lys Val Asp Ser Ile Ser Tyr Asn Ile Gln		
198		290	295 300
199			
200	Asn Arg Glu Trp Tyr Ile Pro Leu Pro Ser His Ile Met Thr Lys Gly		
201		305	310 315 320
202			
203	Ala Phe Leu Gly Gly Ala Asp Val Lys Glu Cys Ile Glu Ala Phe Ser		
204		325	330 335
205			

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206 Ser Tyr Ile Cys Pro Ser Asp Pro Gly Phe Val Leu Asn His Glu Met
207           340           345           350
208
209 Glu Ser Cys Leu Ser Gly Asn Ile Ser Gln Cys Pro Arg Thr Thr Val
210           355           360           365
211
212 Thr Ser Asp Ile Val Pro Arg Tyr Ala Phe Val Asn Gly Gly Val Val
213           370           375           380
214
215 Ala Asn Cys Ile Thr Thr Thr Cys Thr Cys Asn Gly Ile Asp Asn Arg
216           385           390           395           400
217
218 Ile Asn Gln Pro Pro Asp Gln Gly Val Lys Ile Ile Thr His Lys Glu
219           405           410           415
220
221 Cys Asn Thr Ile Gly Ile Asn Gly Met Leu Phe Asn Thr Asn Lys Glu
222           420           425           430
223
224 Gly Thr Leu Ala Phe Tyr Thr Pro Asn Asp Ile Thr Leu Asn Asn Ser
225           435           440           445
226
227 Val Ala Leu Asp Pro Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys
228           450           455           460
229
230 Ser Asp Leu Glu Glu Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys
231           465           470           475           480
232
233 Leu Asp Ser Ile Gly Asn Trp His Gln Ser Ser Thr Thr Ile Ile Ile
234           485           490           495
235
236 Ile Leu Ile Met Ile Ile Ile Leu Phe Ile Ile Asn Val Thr Ile Ile
237           500           505           510
238
239 Thr Ile Ala Ile Lys Tyr Tyr Arg Ile Gln Lys Arg Asn Arg Val Asp
240           515           520           525
241
242 Gln Asn Asp Lys Pro Tyr Val Leu Thr Asn Lys
243           530           535
244
245

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

256 AGACAAATCC AAATTCGAGA TGAATACTG GAAGCATACC AATCACGGAA AGGATGCTGG

60

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Original Text